



PCT

## RAW SEQUENCE LISTING

DATE: 04/03/2003

PATENT APPLICATION: US/10/030,269A

TIME: 14:28:06

Input Set : A:\217925US0XPCT.txt

Output Set: N:\CRF4\04032003\J030269A.raw

3 <110> APPLICANT: OTA, TOSHIO  
 4 ISOGAI, TAKAO  
 5 NISHIKAWA, TETSUO  
 6 HIO, YURI  
 7 YAMAZAKI, MAYAKO  
 8 SATOH, SUSUMU  
 9 ARAKAWA, HIROYUKI  
 10 MORITA, MASAHIKO  
 12 <120> TITLE OF INVENTION: AMYLOID-BETA PROTEIN AGGREGATION-REGULATING FACTORS  
 14 <130> FILE REFERENCE: 217925US0XPCT  
 16 <140> CURRENT APPLICATION NUMBER: 10/030,269A  
 C--> 17 <141> CURRENT FILING DATE: 2002-09-09  
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP00/04515  
 20 <151> PRIOR FILING DATE: 2000-07-06  
 22 <150> PRIOR APPLICATION NUMBER: JP 11-194179  
 23 <151> PRIOR FILING DATE: 1999-07-08  
 25 <150> PRIOR APPLICATION NUMBER: US 60/159,586  
 26 <151> PRIOR FILING DATE: 1999-10-18  
 28 <160> NUMBER OF SEQ ID NOS: 22  
 30 <170> SOFTWARE: PatentIn version 3.1  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 1499  
 34 <212> TYPE: DNA  
 35 <213> ORGANISM: Homo sapiens  
 37 <220> FEATURE:  
 38 <221> NAME/KEY: CDS  
 39 <222> LOCATION: (58)..(606)  
 40 <223> OTHER INFORMATION:  
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 46 atg aag ctc tta tct ttg gtg gcc gtg gtc ggg tgt ttg ctg gtg ccc 105  
 47 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
 48 1 5 10 15  
 50 cca gct gaa gcc aac aag agt tct gaa gat atc cggtgc aaa tgc atc 153  
 51 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile  
 52 20 25 30  
 54 tgt cca cct tat aga aac atc agt ggg cat att tac aac cag aat gta 201  
 55 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
 56 35 40 45  
 58 tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 249  
 59 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
 60 50 55 60  
 62 cct gcc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 297

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Input Set : A:\217925US0XPT.txt

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64 65 70 75 80
66 gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 345
67 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
68 85 90 95
70 tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 393
71 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
72 100 105 110
74 gac cct ctg atc cga aag ccg gat gca tac act gag caa ctg cac aat 441
75 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
76 115 120 125
78 gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 489
79 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
80 130 135 140
82 ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 537
83 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
84 145 150 155 160
86 cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 585
87 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
88 165 170 175
90 gat cgg cac aag atg ctc agc tagatgggct ggtgtggtt ggtaaggcc 636
91 Asp Arg His Lys Met Leu Ser
92 180
94 ccaacaccat ggctgccagc ttccaggctg gacaagcag ggggtactt ctcccttccc 696
96 tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctcccttccc ctaactttag 756
98 aaatgttgtta ctgtgctatt ttgattaggg aagagggatg ttgtctctga tctctgttgt 816
100 ctctctgggt ctgtggggtt gaagggatgg ggaaggcagg ccagaaggga atggagacat 876
102 tcgaggcggc ctcaaggatg gatgcgatct gtctctcctg gctccactct tgccgccttc 936
104 cagctctcag tcttgggaat gttgttacc ttggaagata aagctgggtc ttcaggaact 996
106 cagtgtctgg gaggaaagca tggcccagca ttcacgatgt gttccttttc gcagtgtgtt 1056
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116 tgtccacagt cactgagcca gacggtcggt tggaacatga gactcgagc tgagcgtgga 1356
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122 cattaaattg tttttttct ctc 1499
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 183
127 <212> TYPE: PRT
128 <213> ORGANISM: Homo sapiens
129 <400> SEQUENCE: 2
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133 1 5 10 15
136 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
137 20 25 30
140 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
141 35 40 45

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Input Set : A:\217925US0XPCT.txt

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144 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
145      50      55      60
148 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Cys Glu Cys Arg Tyr
149 65      70      75      80
152 Glu Glu Arg Ser Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
153      85      90      95
156 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
157      100      105      110
160 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
161      115      120      125
164 Gln Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
165      130      135      140
168 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
169 145      150      155      160
172 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Arg Lys Thr Val Phe
173      165      170      175
176 Asp Arg His Lys Met Leu Ser
177      180
180 <210> SEQ ID NO: 3
181 <211> LENGTH: 1828
182 <212> TYPE: DNA
183 <213> ORGANISM: Homo sapiens
185 <220> FEATURE:
186 <221> NAME/KEY: CDS
187 <222> LOCATION: (83)..(487)
188 <223> OTHER INFORMATION:
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194 gggcgacgtg cccgcttcca aa atg gcg gcg gcg gta tct ggt gcg ctt 112
195      Met Ala Ala Ala Val Ser Gly Ala Leu
196      1      5      10
198 ggc cgg gcg gcc tgg agg ctg ctg cag ctg cga tgc ctg ccc gtg gcc 160
199 Gly Arg Ala Gly Trp Arg Leu Leu Gln Leu Arg Cys Leu Pro Val Ala
200      15      20      25
202 cgt tgc cga caa gcc ctg gtg ccg cgt gcc ttc cat gct tca gct gtg 208
203 Arg Cys Arg Gln Ala Leu Val Pro Arg Ala Phe His Ala Ser Ala Val
204      30      35      40
206 ggg cta agg tct tca gat gag cag aag cag cag cct ccc aac tca ttt 256
207 Gly Leu Arg Ser Ser Asp Glu Gln Lys Gln Gln Pro Pro Asn Ser Phe
208      45      50      55
210 tct cag cag cat tct gag aca cag ggc gca gaa aaa cct gat cca gag 304
211 Ser Gln Gln His Ser Glu Thr Gln Gly Ala Glu Lys Pro Asp Pro Glu
212      60      65      70
214 tct tct cat tca ccc ccc agg tat aca gac cag ggc ggc gag gag gag 352
215 Ser Ser His Ser Pro Pro Arg Tyr Thr Asp Gln Gly Gly Glu Glu Glu
216 75      80      85      90
218 gag gac tat gaa agt gag gag cag ttg cag cac cgc atc ctg acg gca 400
219 Glu Asp Tyr Glu Ser Glu Glu Gln Leu Gln His Arg Ile Leu Thr Ala
220      95      100      105

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Input Set : A:\217925US0XPCT.txt

Output Set : N:\CRF4\04032003\J030269A.raw

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222 gcc ctt gag ttt gtg ccc gcc cac ggg tgg aca gca gag gcg att gca      448
223 Ala Leu Glu Phe Val Pro Ala His Gly Trp Thr Ala Glu Ala Ile Ala
224      110      115      120
226 gaa gga gcc cag gtg tgt ata ggt gag ggt ggg gcc acc taaccaagat      497
227 Glu Gly Ala Gln Val Cys Ile Gly Glu Gly Gly Ala Thr
228      125      130      135
230 gagccaggat ggagtcacac caggcagagc ggggggcctc atgccttctt ccagcttagc      557
232 tcagagcccc tcacagctgc aagattgact ggtttttttc cccaatagg gtggaactgg      617
234 cttttatttg tagttataaa gaacatacca tggagttggt tcttgggagt tegtgtcttaa      677
236 aggcacatcta ttaggcaaga attgtctgtg atcaaaactc ccatgtttca ttgactctaa      737
238 gatgccattg ttgttaagaa gcatcatttl laaaalgcatc agtaaaaaag aaacatact      797
240 gcccttcgaa ctatgacaaa gcactttctg gattcacact gattttttaa aatgaaaaat      857
242 atatctgcat cttagaatta atgacatatg gtgtttgaaa accccaaga aggcaccact      917
244 ttggagacca acacatctta ttttcccgaa aactctaata gcattttctg cattagtaca      977
246 gactgtctgt ttagatttag cagcaggctc atgttcaggc catgttgtag agaactctcc      1037
248 agcatagcaa gataccatcc tccaagagac tgaggggatg acagagttgc atcttccatc      1097
250 ccaggcttgc tgcaggcgat ctacccatgg acaatgggca aggttctctc ttacttgaaa      1157
252 tttaaactgt atttccttgt ctctctcacc tcccaagtgc acatttggtg acagaagtct      1217
254 cttagtgaag attgtgggtgc tctgactcca atgtgagctc atgtgacaaa ctgaacacta      1277
256 caaacaataa taataaaagaa tgtagaanaac acctataatc acaccaaga tcatactatc      1337
258 aacatttatg cctagatctt tccaattaaa accctttata tgattcattc tttaaatgtt      1397
260 tattgagcaa ataattgtcc ctaggcactg tgctagtcca agagacatga cagggggtcaa      1457
262 agtggccaag atggatctgc ttctctgcct tggtgagctt ccagctctagc aacatttaata      1517
264 aaatatatac aaatgtttac ttagaagatg tggttaagtgc tatcaaggaa aggtgtctgt      1577
266 gggctgtata atggagggac ccgatcatta gatcaggtea cagctgcgag attgactggt      1637
268 ttctttccct caatagggtg gaaatggctt tattttgtgg atataaaagt aatgaacct      1697
270 ggaattggtt cttgagagtt gtgttctaaa ggcaacctat tggcaagaat tgtctgtgat      1757
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274 agtacatcag t
277 <210> SEQ ID NO: 4
278 <211> LENGTH: 135
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapiens
282 <400> SEQUENCE: 4
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285 1      5      10      15
288 Leu Leu Gln Leu Arg Cys Leu Pro Val Ala Arg Cys Arg Gln Ala Leu
289      20      25      30
292 Val Pro Arg Ala Phe His Ala Ser Ala Val Gly Leu Arg Ser Ser Asp
293      35      40      45
296 Glu Gln Lys Gln Gln Pro Pro Asn Ser Phe Ser Gln Gln His Ser Glu
297      50      55      60
300 Thr Gln Gly Ala Gln Lys Pro Asp Pro Glu Ser Ser His Ser Pro Pro
301 65      70      75      80
304 Arg Tyr Thr Asp Gln Gly Gly Glu Glu Glu Glu Asp Tyr Glu Ser Glu
305      85      90      95
308 Glu Gln Leu Gln His Arg Ile Leu Thr Ala Ala Leu Glu Phe Val Pro
309      100      105      110
312 Ala His Gly Trp Thr Ala Glu Ala Ile Ala Glu Gly Ala Gln Val Cys

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Input Set : A:\217925US0XPCT.txt

Output Set : N:\CRF4\04032003\J030269A.raw

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136 Ile Gly Glu Gly Gly Ala Thr
137          130          135
320 <210> SEQ ID NO: 5
321 <211> LENGTH: 1584
322 <212> TYPE: DNA
323 <213> ORGANISM: Homo sapiens
325 <220> FEATURE:
326 <221> NAME/KEY: CDS
327 <222> LOCATION: (100)..(1194)
328 <223> OTHER INFORMATION:
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334 tcgccccctg cccacccggg cggccgtagg gcggtcacg atg ctg ccg ccc tta 114
335                                     Met Leu Pro Pro Leu
336                                     1 5
338 ccc tcc cgc ctg ggg ctg ctg ctg ctg ctg tgc ccg gcg cac 162
339 Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Cys Pro Ala His
340                                     10 15 20
342 gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc ttg gtt atg gac cct 210
343 Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro Leu Val Met Asp Pro
344                                     25 30 35
346 acc agc atc tgc agg aag gca cgg cgg ctg gcc ggg cgg cag gcc gag 258
347 Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala Gly Arg Gln Ala Glu
348                                     40 45 50
350 ttg tgc cag gct gag ccg gaa gtg gtg gca gag cta gct cgg gcc gcc 306
351 Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu Leu Ala Arg Gly Ala
352                                     55 60 65
354 cgg ctg ggg gtg cga gag tgc cag ttc cag ttc cgc ttc cgc cgc tgg 354
355 Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe Arg Phe Arg Arg Trp
356 70                                     75 80 85
358 aat tgc tcc agc cac agc aag gcc ttt gga cgc atc ctg caa cag gac 402
359 Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg Ile Leu Gln Gln Asp
360                                     90 95 100
362 att cgg gag acg gcc ttc gtg ttc gcc atc act gcg gcc gcc gcc gcc 450
363 Ile Arg Glu Thr Ala Phe Val Phe Ala Ile Thr Ala Ala Gly Ala Ser
364                                     105 110 115
366 cac gcc gtc acg cag gcc tgt tct atg ggc gag ctg ctg cag tgc gcc 498
367 His Ala Val Thr Gln Ala Cys Ser Met Gly Glu Leu Leu Gln Cys Gly
368                                     120 125 130
370 tgc cag gcg ccc cgc tgg cgg gcc cct ccc cgg ccc tcc gcc ctg ccc 546
371 Cys Gln Ala Pro Arg Trp Arg Ala Pro Pro Arg Pro Ser Gly Leu Pro
372                                     135 140 145
374 gcc acc ccc gga ccc cct gcc gcc gcc gcc gcc tcc gaa gcc agc gcc 594
375 Gly Thr Pro Gly Pro Pro Gly Pro Ala Gly Ser Pro Glu Gly Ser Ala
376 150                                     155 160 165
378 gcc tgg gag tgg gga gcc tgc gcc gac gac gtg gac ttc ggg gac gag 642
379 Ala Trp Glu Trp Gly Gly Cys Gly Asp Asp Val Asp Phe Gly Asp Glu
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/030,269A

DATE: 04/03/2003

TIME: 14:28:07

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Output Set: N:\CRF4\04032003\J030269A.raw

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L:331 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:328  
L:553 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:550  
L:841 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:838